

		Matches	27; Conservative	106; Mismatches	85; Indels	3; Gaps	3;
BASE COUNT	7 a	19	WMMKHTMMTBWCCVRRVGTNNKGHRRTTWWCDNSDHACRYTVBWWYKRGYGYG	78			
ORIGIN	/lab-host="E. coli SOLR"	16 c	21 g	34 t	169 others		
Query Match	Best Local Similarity 1.9%; Score 53; DB 17; Length 247; /tissue-type="Immature Seed" /dev-stage="5 days after pollination"						
Matches	21; Conservative 12.8%; Pred. No. 2.90e-41; Mismatches 58; Indels 1; Gaps 1; /tissue-type="Immature Seed" /dev-stage="5 days after pollination"	21	a	21	9	34	t
RESULT	4	AA754458	247 bp	mRNA	EST	20-JAN-1998	
LOCUS	97SN1784	Rice Immature Seed Lambda ZAPII cDNA Library	Oryza sativa				
DEFINITION	97SN1784	Rice Immature Seed Lambda ZAPII cDNA Library	Oryza sativa				
ACCESSION	AA754458	CDNA clone 97SN1784, mRNA sequence.					
NID	92801164						
VERSION	AA754458.1	GI:2801164					
KEYWORDS	EST.						
SOURCE	ORGANISM	Oryza sativa.					
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.							
REFERENCE	1	(bases 1 to 247)					
AUTHORS	Nahn,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Rahn,T.R., Moon,E.P., Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y., Lee,M.C. and Eun,M.Y.						
TITLE	Larvae-scale Sequencing Analysis of ESTs from Rice Immature Seed						
JOURNAL	Unpublished (1998)						
COMMENT	On Jan 14, 1998 this sequence version replaced 91:1797455.						
Contact: Eun M.Y.							
Department of Cytogenetics							
National Inst. of Agric. Sci. and Tech., RDA							
Suwon, Kyunggi-do, Korea							
Tel: 82 331 290 0301							
Fax: 82 331 290 0307							
Email: myeun@sun20.asti.re.kr							
Submitted by Baek Hie Nahn, Dept. of Biological Science, Myongji University, Yongin, Korea, 449-728 bhnahn@biobserver.myongji.ac.kr							
Seq Primer: M13 Reverse Primer.							
Location/Qualifiers							
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/cultivar="Milayang23"							
/note="Vector: pBluscript SK(+); Site_1: EcoRI; Site_2: XbaI; Directional cDNA library inserted into lambda ZAPII vector at 5' end with EcoRI and 3' end with Xba I site."							
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/map="6"							
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Best Local Similarity 12.2%; Pred. No. 3.91e-35; /tissue-type="Leaf Primordia" /dev-stage="P7-P11 Leaf"	16 c	21 g	34 t	169 others			
BASE COUNT	7 a	16 c	21 g	34 t	169 others		
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Best Local Similarity 12.2%; Pred. No. 3.91e-35; /tissue-type="Leaf Primordia" /dev-stage="P7-P11 Leaf"	16 c	21 g	34 t	169 others			
BASE COUNT	7 a	16 c	21 g	34 t	169 others		
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Best Local Similarity 63.1%; Pred. No. 1.05e-27; Mismatches 80; Indels 3; Gaps 2; /tissue-type="Leaf Primordia" /dev-stage="P7-P11 Leaf" /lab-host="E. coli XLI-Blue MFR"	142 c	142 t	142 a	142 g	142 others		
BASE COUNT	7 a	16 c	21 g	34 t	169 others		
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BASE COUNT	7 a	16 c	21 g	34 t	169 others		
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BASE COUNT	7 a	16 c	21 g	34 t	169 others		
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ORIGIN							
Query Match	Best Local Similarity 1.6%; Score 44; DB 27; Length 656; /tissue-type="Leaf Primordia" /dev-stage="P7-P11 Leaf" /lab-host="E. coli XLI-Blue MFR"						
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Contact: *Tripodis*, Nikos
 Division of Medical and Molecular Genetics
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pRT3
 vector. This library is the normalized version of
 NCI-*CGAP*_Br1. Library was constructed by Bento Soares
 and M. Fatima Bonaldo. "Location/Qualifiers
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 Db 1537 YTSTYKSWRWWYTYTYWWCWCCSTMKSASCANRWMYMGSSRSSTWGSMS 1595
 Cp 1301 tagttttcagaataatgatactcacatggccaaaaaacaagtttgccca 1242
 Db 1596 GCYGMWTKRYRYSWGTWKTWYW 1620
 Cp 1241 caaactgtatcgatggccataatc 1217
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 NID 9255312
 VERSION AA633452.1
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 SOURCE
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 301).
 AUTHORS NCI-*CGAP* http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT On Sep 12, 1996 this sequence version replaced g1:1397573.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-*CGAP* clone distribution information can be
 found through the I.M.A.G.E. Consortium/LIN at:
 www.bio.llnl.gov/bbrp/image/image.html
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 Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
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 [5'-
 TGTACCAATGAACTGGAGCCGCCCCACCAATTGTTTTTTTTTTTTTT
 T-3']/ double-stranded cDNA was size selected, ligated to
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 cloned into the Not I and Eco RI sites of a modified pRT3
 vector (Pharmacia). Library went through one round of
 normalization to a *cot* = 5. Library constructed by Bento
 Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid
 adenomas was kindly provided by Dr. Stephen Marx. National
 Institutes of Health, Bethesda, MD
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 and M. Fatima Bonaldo. "Location/Qualifiers
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 Cq 114 acaaaaaattcacgcgcctacaacattacaatatgttcaaataagactaa 170
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 NID 9292637
 VERSION AA846497.1
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 301).
 AUTHORS NCI-*CGAP* http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT On Jan 19, 1998 this sequence version replaced g1:2151145.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-*CGAP* clone distribution information can be
 found through the I.M.A.G.E. Consortium/LIN at:
 www.bio.llnl.gov/bbrp/image/image.html
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 Seq primer: -10m13 fwd. ET from Amersham
 High quality sequence stop: 279.
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 (Pharmacia) with a modified polylinker; Site_1: Not I;
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 [5'-
 TGTACCAATGAACTGGAGCCGCCCCACCAATTGTTTTTTTTTTTT
 T-3']/ double-stranded cDNA was size selected, ligated to
 Eco RI adaptors (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of a modified pRT3
 vector (Pharmacia). Library went through one round of
 normalization to a *cot* = 5. Library constructed by Bento
 Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid
 adenomas was kindly provided by Dr. Stephen Marx. National
 Institutes of Health, Bethesda, MD
 Insert Length: 1859 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 151.
 FEATURES source
 1. .250
 /organism="Homo sapiens"
 /note="Vector: pRT73D-Pac (Pharmacia) with a modified
 polylinker; 1st strand cDNA was prepared from pooled bulk
 breast tumor tissue, and was then primed with a Not I -

